

Introduction

Traditional phylogenetic methods have yet to uncover exactly how and when the modern coral reef fish fauna evolved. The majority of reef fish families fall within the group Percomorpha. Higher resolution in comparative studies of percomorph fishes would require the generation of datasets that sample large numbers of both taxa and genetic loci. **DNA ultraconserved elements (UCEs)** are highly conserved genomic regions that have been identified in deeply divergent taxa (Bejerano et al. 2004). Sequence capture and targeted enrichment of UCEs offer an efficient and economical way to generate large datasets for phylogenomic analysis.

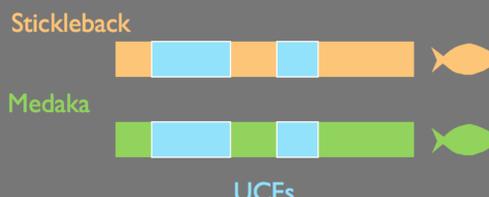
Objective

To generate the first phylogenomic hypothesis for percomorph fishes using UCEs.

Results

Percomorph Capture Array

a. Identification of UCEs



b. In silico probe design



c. In vivo target enrichment of UCEs

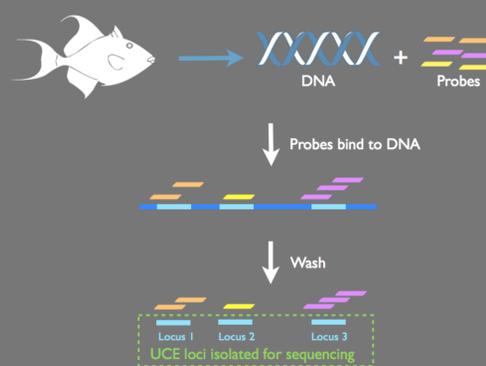
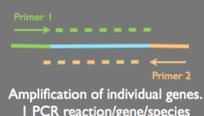


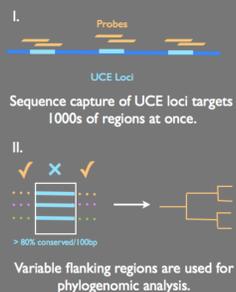
Figure 1 (a,b,c) Identification of percomorph-specific UCEs and in vitro target enrichment using custom RNA probes. Post-sequencing alignment and processing was performed using LASTZ and PHYLUCE.

Generating datasets for comparative analysis

Traditional Methods



UCEs Method



Research Questions

- Can UCEs function as informative phylogenomic markers in coral reef fishes?
- Can UCEs be used to resolve relationships both within and among percomorphs?
- Are recently proposed relationships using traditional markers recovered?

Final Dataset

- 58 taxa, 46 families
- ~ 1300 UCE loci
- 50-100X coverage per locus

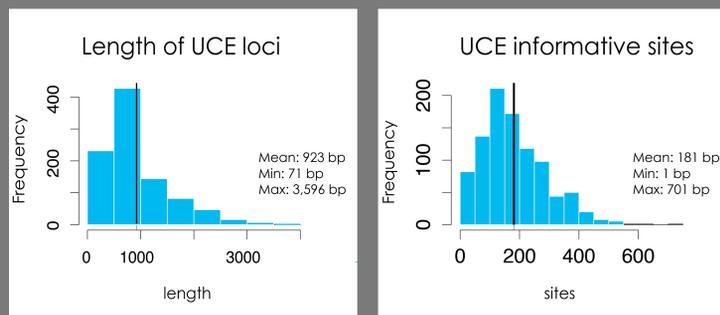


Figure 2 Summary statistics for the final UCE dataset for percomorphs. Only loci recovered in at least 75% of the taxa were included in alignments.

a. Phylogram of Species

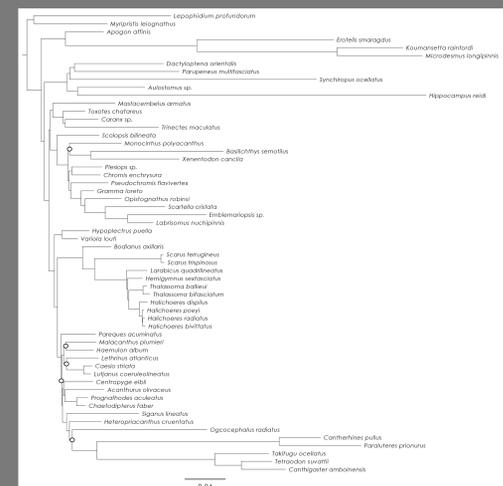
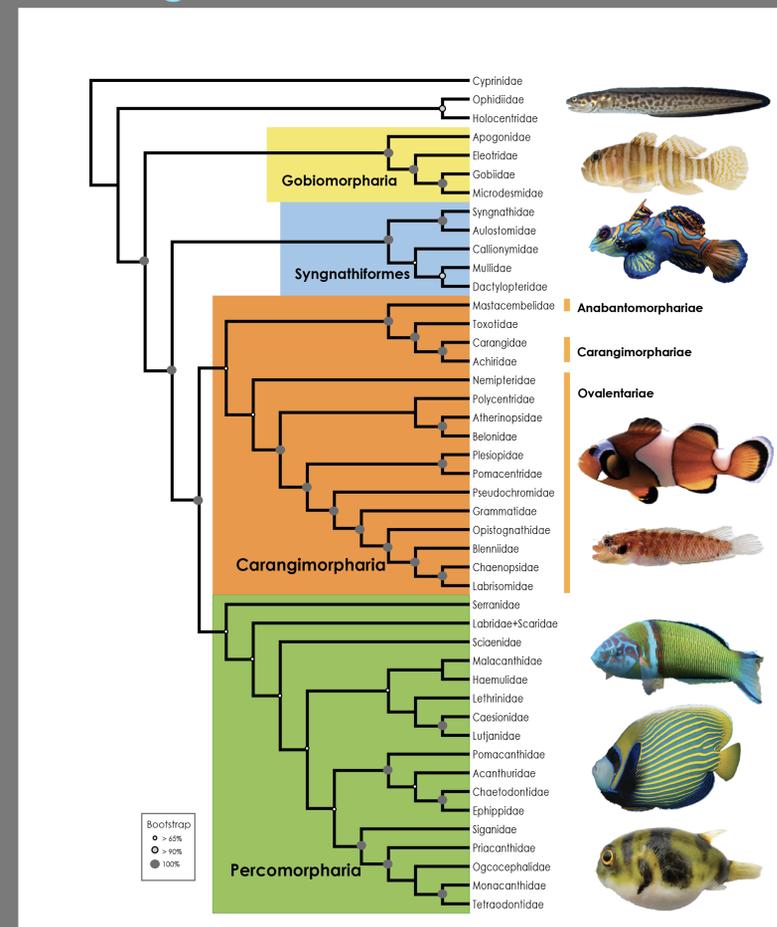


Figure 3 Final tree of 52 percomorph fishes inferred from ~1300 UCE loci using maximum likelihood and assessed through bootstrap analysis in RAxML.

(a) Phylogram of all species sampled. Branch lengths are drawn to scale. Tree is rooted with *Danio rerio* (not shown). Support for nodes is >65% except where indicated.

(b) Cladogram showing sampled families. Major groups proposed in Betancur-R. et al. 2013 are indicated in bold.

b. Cladogram of Families



Conclusions

- UCEs recover 7/9 percomorph lineages proposed in Betancur-R. et al. 2013 with high support
- UCEs can be used as phylogenomic markers in non-amniotes.

References

- A Phylogenomic Perspective on the Radiation of Ray-Finned Fishes Based upon Targeted Sequencing of Ultraconserved Elements (UCEs) Faircloth BC, Sorenson L, Santini F, Alfaro ME (2013) PLoS ONE 8(6): e65923. doi:10.1371/journal.pone.0065923
- Ultraconserved elements anchor thousands of genetic markers spanning multiple evolutionary timescales BC Faircloth, JE McCormack, NG Crawford, MG Harvey, RT Brumfield, TC Glenn Systematic biology 61 (5), 717-726

